

GenCore version 4.5  
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1 nucleic - nucleic search, using sw model

on: February 5, 2002, 16:26:13 : Search time 3596.51 Seconds  
(without alignments)  
2456.000 Million cell updates/sec

File: US-09-509-591-1

Project score: 822  
Sequence: 1 GCATCTGCTGCACTCTGTA.....TTCCACCACTGCAATATACA 822

Indexing table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Number of hits satisfying chosen parameters: 22703874

num DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: EST:

- 1: em\_estfun:\*
- 2: em\_estfun:\*
- 3: em\_estfun:\*
- 4: em\_estfun:\*
- 5: em\_estfun:\*
- 6: em\_estfun:\*
- 7: em\_estfun:\*
- 8: em\_estfun:\*
- 9: em\_estfun:\*
- 10: em\_estfun:\*
- 11: em\_estfun:\*
- 12: em\_estfun:\*
- 13: em\_estfun:\*
- 14: em\_estfun:\*
- 15: em\_estfun:\*
- 16: em\_estfun:\*
- 17: em\_estfun:\*
- 18: em\_estfun:\*
- 19: em\_estfun:\*
- 20: em\_estfun:\*
- 21: em\_estfun:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed  
and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Match	Length	ID
1	197.2	24.0	556	A0005402
2	85	10.3	873	A0121310
3	52.2	6.4	1101	CNS0100X
4	51.2	6.2	574	A0838165
5	47	5.7	456	BF770244
6	46.4	5.6	553	A0542774
7	46.2	5.6	749	A0743299
8	45.4	5.5	534	BF770233
9	44.6	5.4	1101	CNS0039G
10	44.2	5.3	364	A0248096
11	43.8	5.3	364	AA587883
12	43.8	5.3	417	BF773316

Result No.	Score	Match	Length	ID	Description
1	197.2	24.0	556	A0005402	CITR-HSP
2	85	10.3	873	A0121310	A0121310
3	52.2	6.4	1101	CNS0100X	A0988379
4	51.2	6.2	574	A0838165	HS-1712A
5	47	5.7	456	BF770244	RC3-IT002
6	46.4	5.6	553	A0542774	RC3-IT002
7	46.2	5.6	749	A0743299	HS-387
8	45.4	5.5	534	BF770233	RC3-IT002
9	44.6	5.4	1101	CNS0039G	A063921
10	44.2	5.3	364	A0248096	HS-2015A
11	43.8	5.3	364	AA587883	nm714051
12	43.8	5.3	417	BF773316	CM3-IT002

Result No.	Score	Match	Length	ID	Description
13	43.8	5.3	450	A1392863	tg05a08.x
14	43.8	5.3	492	AM614814	hg80a02.x
15	43.2	5.3	360	B65091	CITR-HSP-201
16	42.6	5.2	489	A0427571	CITR-BL
17	42.6	5.2	587	B95393	CITR-HSP-216
18	42.4	5.2	347	A0665278	HS-5360_A
19	42	5.1	797	CNS003F8	A064634
20	42	5.1	1101	CNS002M0	Drosophila
21	41.8	5.1	417	A0204327	HS-3113_B
22	41.8	5.1	483	A031643	RC3-IT002
23	41.8	5.1	588	B48698	RC3-IT002
24	41.6	5.1	1101	CNS00238	A097166
25	41.2	5.0	537	BF003883	EST43281
26	41.2	5.0	714	A0377558	RC3-IT002
27	41.2	5.0	1101	CNS00EFA	A069119
28	41.2	5.0	1101	CNS00FDC	A070547
29	41.1	5.0	341	A0104872	HS-216_B
30	41.1	5.0	439	AA790739	VR82912.r
31	41.1	5.0	1101	CNS016L1	A106896
32	41.1	5.0	1201	CNS01522	Drosophila
33	40.8	5.0	437	AA622800	np7708.s
34	40.6	4.9	600	A1830342	w159d12.x
35	40.4	4.9	584	A0372805	RC3-IT002
36	40.4	4.9	928	CNS00DKY	A071865
37	40.4	4.9	1085	CNS007GH	A1067540
38	40.4	4.9	1101	CNS017KX	Drosophila
39	40.2	4.9	544	A0429595	CITR-BL
40	40.2	4.9	548	BE030762	128942_MA
41	40.2	4.9	859	CNS00KIL	AL077728
42	40	4.9	359	BB889090	601513532
43	40	4.9	590	A0551355	RC3-IT002
44	40	4.9	876	A5527553	RC3-IT002
45	40	4.9	920	A2529784	ENTB24TF

ALIGNMENTS

RESULT: 1  
LOCUS: A0005402/C  
DEFINITION: CITR-HSP-229362.TF CITR-HSP Homo sapiens genomic clone 229362, DNA  
ACCESSION: A0005402  
VERSION: A0005402.1 GI:3082847  
KEYWORDS: GSS  
SOURCE: human  
ORGANISM: Homo sapiens  
REFERENCE: 1 (bases 1 to 556)  
AUTHORS: Adams M.D., Rounsley S.D., Zhao S., Field C.E., Baas S., Linher K., Golden K., Berry K., Granger D., Suh E., Wible C., Shizuya H., Simon M. and Venter J.C.  
TITLE: Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)  
JOURNAL: Unpublished (1998)  
COMMENT: Contact: Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9711 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: madams@igf.org  
Closes are available from Research Genetics (info@resgen.com). BAC  
ends are available from Research Genetics (info@resgen.com). BAC  
Seq Primer: 113-21:  
Class: BAC ends  
Location: Qualifiers  
Source: 1: 556  
Organization: "Homo sapiens"  
db\_xref: "GDB:7151790"

912 | ИСТНАСТАНЧСТМАУММУМНМ

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                                /sex="Male"
                                /note="Organ: sperm; Vector: pBel0Bac11; BAC clones in
                                E-coli DH10B"
BASE COUNT      171 a      123 c      84 g      177 t      19 others
ORIGIN
Query Match      6128; Score 51.2; DB 13; Length 574;
Best Local Similarity 63.1%; Pred. No. 0.21;
Matches: 94; Conservative 0; Mismatches 54; Indels 1; Gaps 1;
OY 133 TCTTCAGGTTCTCTTTTCAGCTGCTACCTA-TTTTCTCAGCAGCTACATGGCTACAA 191
Db 367 TCTTCAGCTTTTCACTGATACCTCTATCTTCTATCTTACCTTACAGCTCATGGCTTTAA 426
OY 192 TAACTGCTCGAACCTTATGATTCCTCAATTCATCTCTAGCCCTCAATCTTGGTTCAGA 251
Db 427 ATACCACTCTCAACTATGATGACTTTCAANAATTAAGCTCCAGCTTGATCTGAACTCAGA 486
OY 252 AGATTAAAGTAGTATTTCAATGCACATC 280
Db 487 ATGTACTATGTAGCTTCTTACTAGACATC 515

RESULT 5
BE770244/c BE770244 456 bp mRNA EST 12-JAN-2001
LOCUS RC3-IT0022-2011000-021-812 IT0022 Homo sapiens CDNA, mRNA sequence.
DEFINITION BE770244
ACCESSION BE770244.1 GI:12118144
VERSION EST
KEYWORDS
SOURCE human

```

REFERENCE 1. (base) 10 to 456)

AUTHORS Mammalia, Eutheria; Primates; Catarrhini; Hominoidea; Homo.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202631

COMMENT Contact: Simpson, A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rm Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2700922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/ICR Human Cancer Genome Project. This entry can be seen in the following URL  
<http://www.ludwig.org.br/scripts/gethtml2.pl?rl=KC3at2-KC3-IT0022>  
201006021 p12a53-2000-11-20a54-1)  
Seq Primer: puc 18 forward  
High quality sequence start: 17  
High quality sequence stop: 454  
Location/Qualifiers  
1. 455  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_id="IT0022"  
/dev\_stage="Adult"

/note="Organ: epid.tumor; Vector: puc18; site1: Sma1;  
 site\_2: Sma1; A mini-library was made by cloning products  
 derived from ORSITES PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 phorbols into the pUC 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under

BASE COUNT 166 a 55 c 130 g 103 t  
 ORIGIN

Query Match 5.7%; Score 47; DB 11; Length 456;  
 Best Local Similarity 58.0%; Pred. No. 1.8;  
 Matches 83; Conservative 0; Mismatches 60; Indels 0; Gaps 0

2Y 182 ATGGTCACATTAACCTGTGCAAGCTTATGATCCCAATATATCTAGCCTCAATC 211  
 2Y 317 ATAGATTTCAATGCCATTTCTATGATCAATGACCTTCAATCTCAATCCGCCATTC 258  
 2Y 242 TTCTTCACAGAGATTAAGATATATTCATATGACATCAAGCTTCAATGGAGGCT 301  
 2Y 257 TTGTGCTGTGAACCTAGACACACATCTAGAGAGCTTTTGGACATCTCCACTAGACCTTC 198  
 302 TAAAGAGCTTCAACATACAAAC 324  
 197 CACAGACATCTCAGATCCGAAC 175

RESULT 6  
 LOCUS AO542774 553 bp DNA 16-JUL-1999  
 DEFINITION RPCI-11-361L13.TV RPCI-11 Homo sapiens genomic clone RPCI-11-361L13  
 ' DNA sequence.  
 ACCESSION AO542774  
 VERSION AO542774.1 GI:4873230  
 KEYWORDS GSS.

SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 553)  
 AUTHORS Zhao S., Adams M.D., Nierman W., Malek J., de Jong P. and Venter  
 J.C.  
 TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready  
 Map Building  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: hbeef@igf.org

Clones are derived from the human BAC library RPCI-11. For BAC  
 library availability, please contact Pieter de Jong  
 (pieter@dejong.med.bufileo.edu). Clones may be purchased from  
 BACPAC Resources (<http://bacpac.med.bufileo.edu/ordering>) or from  
 Research Genet cs ([http://www.tigr.org/tdb/humgen/bac\\_end\\_search/bac\\_end\\_search.htm](http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.htm)).  
 Seq primer: T7  
 Class: BAC ends.  
 Location/Qualifiers

FEATURES  
 source  
 1. 353  
 /organism="Homo sapiens"  
 /db\_xref="GDB:7638516"  
 /db\_xref="taxon:9606"  
 /clone="RPCI-11-361L13"  
 /clone\_11D="RPCI-11"  
 /sex="Male"  
 /cell\_type="Lymphocytes"  
 /note="Vector: PBAC3.6; site\_1: EcoRI; site\_2: EcoRI;  
 RPCI11 Human Male BAC Library"  
 BASE COUNT 169 a 121 c 84 g 179 t  
 ORIGIN

Query Match 5.6%; Score 46.4; DB 13; Length 553;  
 Best Local Similarity 62.9%; Pred. No. 2.4;  
 Matches 88; Conservative 0; Mismatches 51; Indels 1; Gaps 1

OY 142 TTCTGCTTACCTGCTATCTA-TTTTTCACACCTCAGAGGCTACATACCTCT 200  
 DB 346 TTTCATGTAATCTGCTATCTATCTATCTATCTACCTCAATGCTTTAAATACCTCT 405  
 OY 201 GCAAGCTTATGATCCCAATATCTATCTATCTATCTATCTATCTATCTATCT 260  
 DB 406 CTATGATGATCTTCAATATATATGATCTGATCTGATCTGATCTGATCTGATCT 465  
 OY 261 GATGATATCAATGCAATC 280  
 DB 466 GTAGCTTCTATCTGATC 485

RESULT 7  
 LOCUS AO743299 749 bp DNA 16-JUL-1999  
 DEFINITION HS-5387.B2.A08.SP6.RPCI-11 Human Male BAC Library Homo sapiens  
 genomic clone Plate-963 Col-16 Row-B, DNA sequence.  
 ACCESSION AO743299 GI:5520821  
 VERSION AO743299.1 GI:5520821  
 KEYWORDS GSS.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 749)  
 AUTHORS Mahairas G.G., Wallace J.C., Smith K., Swartzell S., Holzman T.,  
 Kellar A., Shaker R., Furlong J., Young J., Zhao S., Adams M.D. and  
 Hood L.

TITLE Sequence tagged connectors: A sequence approach to mapping and  
 scanning the human genome  
 JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)  
 MEDLINE 99380589  
 COMMENT Contact: Mahairas G.G., Wallace J.C., Hood L.  
 High Throughput Sequencing Center  
 University of Washington  
 401 Queen Anne Avenue North, Seattle, WA 98109, USA  
 Tel: (206) 616-3618  
 Fax: (206) 616-3887  
 Email: j.wallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC  
 library availability, please contact Pieter de Jong  
 (pieter@dejong.med.bufileo.edu). Clones may be purchased from  
 BACPAC Resources (<http://bacpac.med.bufileo.edu/ordering>) or from  
 Research Genet cs ([http://www.tigr.org/tdb/humgen/bac\\_end\\_search/bac\\_end\\_search.htm](http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.htm)).  
 Seq primer: SP6  
 Class: BAC ends.  
 High quality sequence stop: 749.  
 Location/Qualifiers

FEATURES  
 source  
 1. 749  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="Plate-963 Col-16 Row-B"  
 /clone\_11D="RPCI-11 Human Male BAC Library"  
 /sex="Male"  
 /note="Vector: PBAC3.6; site\_1: EcoRI; site\_2: EcoRI;  
 Male blood DNA was isolated from one randomly chosen donor  
 and partially digested with a combination of EcoRI and  
 EcoRI methylase. Site selected DNA was cloned into the  
 PBAC3.6 Vector at EcoRI sites"  
 BASE COUNT 181 a 190 c 166 g 212 t  
 ORIGIN

Query Match 5.6%; Score 46.2; DB 13; Length 749;  
 Best Local Similarity 58.3%; Pred. No. 2.5;  
 Matches 81; Conservative 0; Mismatches 58; Indels 0; Gaps 0

363 CTGGCCATGAGATTAATACAGTTCTTCACGCTTACTGGGTCTTCTGAGGTGGCC 422  
 171 CAACCACTACATGCGCTACATTAACCTCTGCAAGCTTATGATCCCAATATCTATCTC 230  
 423 CAACCACTCCCAATGCGCTCAGATACCTCTGCGCGAGATTCATCAATTTATGCTC 482  
 231 TACCCCAATCTTTGTCCA 249  
 483 CAGGCTAGATGCTTACGA 501

RESULT 8  
 BE770233/534 bp mRNA EST 12-JUN-2001  
 DEFINITION BC3-IT0022-201100-021-c07 IT0022 Homo sapiens cDNA, mRNA sequence.  
 BE770233  
 BE770233 GI:12118133  
 EMBL  
 ORIGIN human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 534)  
 Nagar,M.A., da Silva,W.J., Zago,M.A., Bordin,S., Costa,F.F.,  
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
 Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,  
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
 Simpson,A.J.  
 Shotgun sequencing of the human transcriptome with OBF expressed  
 sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 20202663  
 CONTACT: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LIC Human Cancer Genome  
 Project. This entry can be seen in the following URL:  
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC3ct2-RC3-IT0022-201100-021-c07ct3-2000-11-20ct4-1>)  
 Seq primer: puc 18 forward  
 High quality sequence start: 50  
 High quality sequence stop: 444.  
 Location/Qualifiers  
 1. 534  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_id="IT0022"  
 /dev\_stage="Adult"  
 /note="Organ: epid.tumor; Vector: puc18; Site: Smal; Smal:  
 Site.2: Smal; A mini-library was made by cloning products  
 derived from ORESTES PCR (U.S. Letters/Patent application  
 No. 196/716 - Ludwig Institute for Cancer Research).  
 Profiles into the puc 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."  
 BASE COUNT 191 a 83 c 148 g 112 t

Query Match 5.5; Score 45.4; DB 11; Length 534;  
 Best Local Similarity 57.3; Pred. No. 4;  
 Matches 82; Conservative 0; Mismatches 61; Indels 0; Gaps 0

182 ATGGCTACAAATAGCTGTCGACGCTATGATTCACCAATATCTATCTGAGCCGATC 241  
 350 ATGATGCAATGCAATTCATTCATGATAGGCTTCATCTATCTGAGCCGATC 291

242 TTGTCCAGAGATAAAGATGATTCATCAATGACATCAACATCTCCACTTGGAGGCT 301  
 290 TTGTCTGTAACCTAGAACCAATGATAGAGATTTTGGACATCTCCACTAGACGCTC 231  
 302 TAAAGCGTTTCAACATCAAAC 324  
 230 CACAGACATCTCAGATCCGAAC 208

RESULT 9  
 CNS00396 1101 bp DNA GSS 03-JUN-1999  
 LOCUS  
 DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #  
 BACR08K10 of Fpe1-98 library from Drosophila melanogaster (fruit  
 fly), genomic survey sequence.  
 ACCESSION AL063921  
 VERSION AL063921.1 GI:4941778  
 KEYWORDS GSS.  
 SOURCE fruit fly.  
 ORGANISM Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 1 (bases 1 to 1101)  
 REFERENCES  
 Direct Submission  
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage ;  
 BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
 Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr))  
 Determination of this BAC-end sequence was carried out as part of a  
 collaboration with the Berkeley Drosophila Genome Project (BDGP).  
 The BDGP is constructing a physical map of the Drosophila  
 melanogaster genome using these BACs. For further information  
 please see <http://www.fruitfly.org> The BDGP Drosophila  
 melanogaster BAC library was prepared by Kazuo Ogasawara and  
 Aaron Mamoser in Peter de Jong's laboratory in the Department of  
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,  
 NY. The library is named RPci-98 and was constructed by partial  
 EcoRI digestion of Drosophila DNA provided by the BDGP from the  
 isogenic strain Y2; cn bw sp, the same strain used for the BDGP's  
 pl and EST libraries. A more detailed description of the library  
 and how to order individual BAC clones, the entire library, or  
 filters for hybridization from the BACPAC Resource Center can be  
 found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).  
 Location/Qualifiers  
 1. 1101  
 /organism="Drosophila melanogaster"  
 /db\_xref="taxon:7227"  
 /clone\_id="RPci-98"  
 /clone="BACR08K10"  
 /note="end : TET3"  
 BASE COUNT 201 a 6 c 131 g 202 t 503 others

Query Match 5.4; Score 44.6; DB 13; Length 1101;  
 Best Local Similarity 14.1; Pred. No. 5.5;  
 Matches 57; Conservative 202; Mismatches 142; Indels 2; Gaps 1;

439 GAGAGTGAAGAGGAGCTGATTAATTAATCACTAAGTCAATAGCAGCCAGAC 498  
 756 TTTAAAT 815  
 499 TCTTGCTGAAGCTGACTTATCTTAATTAATATATATATATATATATATATATAT 558  
 816 ATTTAT 873  
 559 TAT 618





```

LOCUS       A192863             450 bp      mRNA                      EST              30-MAR-1999
DEFINITION  hg050802.x1 NCI-CGAP-CL11 Homo sapiens CDNA clone IMAGE:2107862 3',
ACCESSION   A192863
VERSION     A192863
KEYWORDS    EST
SOURCE      human
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 450)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapb@rstat.nlm.nih.gov
            Tissue/Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
            M.D., Louis M. Staudt, M.D., Ph.D.
            CDNA Library Preparation: M. Bento Soares, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone/distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/BLM at:
            www.bio.lnlni.gov/db/rrp/image/image.html
            Insert Length: 1363      Std Error: 0.00
            Seq Primer: -400p from Glbco
            High quality sequence stop: 433.
FEATURES             Location/Qualifiers
     source           1..450
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone IMAGE:2107862"
                     /clone_id="NCI-CGAP-CL11"
                     /tissue_type="B-cell, chronic lymphocytic leukemia"
                     /lab_host="DH10B"
                     /note="Vector: pRT3D-Pac (Pharmacia) with a modified
                     polylinker, site_1: Not I, site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dt) primer [5'
                     TGTTACCAACTGAGTGGGAGCGCGCCGATGCTTTTATTTTTTTTTTTT
                     T 3']; double-stranded cDNA was ligated to Eco RI
                     adaptors (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of the modified pRT3D vector.
                     Library is normalized, and was constructed by Bento
                     Soares and M.Fatima Bonaldio."
BASE COUNT      106 a                55 g                166 t
ORIGIN
106 a
123 c
166 t
Query Match
Best Local Similarity 56.6% Score 43.8 DB 10; Length 450;
Matches 81; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
OY 182 ATGGCTACAATAACGCTGCGAAGTTATGATTTCCCAATATATCTATCTGAGCCCTCATC 241
DB 135 ATAGATTCAATTCGATCTTCATGATTAAGCTTAAATATCTCTATCTCCAGCCCAATTC 194
OY 242 TTGTTCGAGAAGATTAAGATAGTATTCACAAATGCACATCAACGCTCCACTGGAGGCT 301
DB 195 TTGTGCCCGAAGCTCGAATCCACATCTAGAGAAGTTTGTGACATCTCCACTGAGACGTT 254
OY 302 TTAAGACCTTTCACATCAAC 324
DB 255 CACGACATCTCAGATCCGAAC 277
RESULT 14
LOCUS       A192863             452 bp      mRNA                      EST              23-MAR-2000
DEFINITION  hg080802.x1 NCI-CGAP-Kid11 Homo sapiens CDNA clone IMAGE:2951882 3',
ACCESSION   A192863
VERSION     A192863
KEYWORDS    EST
SOURCE      human
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 452)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapb@rstat.nlm.nih.gov
            Tissue/Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
            M.D., Louis M. Staudt, M.D., Ph.D.
            CDNA Library Preparation: M. Bento Soares, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone/distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/BLM at:
            www.bio.lnlni.gov/db/rrp/image/image.html
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                     TGTTACCAACTGAGTGGGAGCGCGCCGATGCTTTTATTTTTTTTTTTT
                     T 3']; double-stranded cDNA was ligated to Eco RI
                     adaptors (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of the modified pRT3D vector.
                     Library is normalized, and was constructed by Bento
                     Soares and M.Fatima Bonaldio."
BASE COUNT      106 a                55 g                166 t
ORIGIN
106 a
123 c
166 t
Query Match
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Matches 81; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
OY 182 ATGGCTACAATAACGCTGCGAAGTTATGATTTCCCAATATATCTATCTGAGCCCTCATC 241
DB 135 ATAGATTCAATTCGATCTTCATGATTAAGCTTAAATATCTCTATCTCCAGCCCAATTC 194
OY 242 TTGTTCGAGAAGATTAAGATAGTATTCACAAATGCACATCAACGCTCCACTGGAGGCT 301
DB 195 TTGTGCCCGAAGCTCGAATCCACATCTAGAGAAGTTTGTGACATCTCCACTGAGACGTT 254
OY 302 TTAAGACCTTTCACATCAAC 324
DB 255 CACGACATCTCAGATCCGAAC 277

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ERSION AM614814.1 GI:7320000  
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 1 (bases 1 to 492)  
 REFERENCE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP)  
 TITLE Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [scapsb-remail.nih.gov](mailto:scapsb-remail.nih.gov)  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: M. Bento Soares, Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LINL at:  
[image.llnl.gov/image/html/Libraries.shtml](http://image.llnl.gov/image/html/Libraries.shtml)  
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 prepared, and ss circles were made in vitro. Following HAP  
 purification, this DNA was used as tracer in a subtractive  
 hybridization reaction. The driver was PCR-amplified cDNAs  
 from a pool of 5,000 clones made from the same library  
 (clonoids 132376-132391, 1456007-1456775, and  
 1500552-1502855). Subtraction by Bento Soares and M.  
 Fatima Bonaldo."  
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 10 GGTTCACAGAGTTCACCTTCCAGAGTCTCTCATCCACCTCCAGGCTCAGGCTACC 69;  
 200 TGCACTTATGATGTCCTCCAAATATCTATCTCTAGCGTCAATCT 242  
 70 TGCGCGACATGATTTTCAATACCAATGCCAGCTCCATCT 112  
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo  
 1 (bases 1 to 360)  
 REFERENCE Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Golden  
 K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M.  
 and Venter,J.C.

TITLE Use of a random BAC End Sequence Database for Sequence-Ready Map  
 Building  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Mark Adams  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: [madams@igf.org](mailto:madams@igf.org)  
 Clones are available from Research Genetics (info@resgen.com). BAC  
 end search page:  
[http://www.tigr.org/tdb/humgen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html)  
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 228 CTCTACCTCAATCTTGTCTCAGAGATATAAAGTAGTATTCAAATGCACATCAAGTCT 287  
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 288 CCACCTGGAGGCTTAAGCGTTTCAACATACAA 323  
 80 CCTTGAATGTTAGTACATCTCAAAATTTGATA 45  
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 Job time: 16830 sec



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